

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:49 ; Search time 32.86 Seconds  
(without alignments)  
123.982 Million cell updates/sec

Title: US-09-331-631A-22\_COPY\_25\_84

Perfect score: 350  
Sequence: 1 EDDNHHNHGHHKSGQCVRRRC.....EKQERSRHEADRSGEGSS 60

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_66:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	350	100.0	122	2 C53234	globulin-10 - maiz
2	350	100.0	582	2 B53234	vicilin-like stora
3	346	98.9	540	2 S21825	vicilin-like stora
4	346	98.9	573	2 A53234	globulin-15, GLB15
5	342	97.7	407	2 T02258	globulin1 - maize
6	303	86.6	236	2 T01662	globulin-1 - maize
7	129.5	37.0	637	2 S35221	globulin Bg1 prec
8	96.5	27.6	1465	2 T23056	hypothetical prote
9	81.5	23.3	605	2 S06398	hypothetical prote
10	78	22.3	494	2 A48133	pre-mRNA splicing
11	74	20.1	971	2 T24866	hypothetical prote
12	71.5	20.4	997	2 T28872	hypothetical prote
13	71	20.3	699	2 A54660	histidine rich cal
14	70	20.0	144	2 F71446	hypothetical prote
15	70	20.0	2339	2 A42566	omega-conotoxin-se
16	69.5	19.9	241	2 S44893	K1236.7 protein -
17	69.5	19.9	361	2 T39008	probable mating pr
18	69.5	19.9	549	2 T17525	proline-rich prote
19	69	19.7	407	1 EDBE03	immediate-early pr
20	69	19.7	588	1 FWCNAB	alpha-globulin B p
21	68.5	19.6	1407	1 S28589	trichoglycin B
22	68.5	19.6	2251	1 B54972	voltage-dependent
23	68.5	19.6	2270	2 A54972	voltage-dependent
24	67.5	19.3	466	2 T18575	cyclophilin isofor
25	67.5	19.3	1196	2 T14108	SH3-containing pro
26	67	19.1	385	2 T19201	hypothetical prote
27	67	19.1	509	2 S08059	alpha-globulin typ
28	67	19.1	566	2 S22477	vicilin precursor
29	67	19.1	897	2 T21688	hypothetical prote

30	66	18.9	2062	2 A59297	myosin X - mouse
31	66	18.9	2237	2 T45115	N-type calcium cha
32	65.5	18.7	480	2 T44225	hypothetical prote
33	65.5	18.7	796	2 JC7355	peroxisome prolif
34	65.5	18.7	2222	2 A37490	voltage-dependent
35	65.5	18.7	2272	2 C54972	voltage-dependent
36	65	18.6	57	2 T16083	hypothetical prote
37	65	18.6	107	2 A29995	protamine p2 precu
38	65	18.6	1105	2 T47582	hypothetical prote
39	65	18.6	1130	2 T30251	repetin - mouse
40	65	18.6	1276	2 T02711	hypothetical prote
41	64	18.3	241	2 T16849	hypothetical prote
42	64	18.3	640	2 A41726	homeotic protein B
43	63.5	18.1	423	2 T43929	DnaJ protein homol
44	63.5	18.1	520	2 S08237	legumin A2 precurs
45	63.5	18.1	763	2 T27620	hypothetical prote

## ALIGNMENTS

RESULT 1  
C53234  
globulin-10 - maize  
C:Species: Zea mays (maize)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 29-Oct-1999  
C:Accession: C53234; S21823  
R:Belanger, F.C.; Kriz, A.L.  
Genetics 129, 863-872, 1991  
A:Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene.  
A:Reference number: A53234; MUID:92090707  
A:Contents: Black Beauty popcorn  
A:Accession: C53234  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-122 <BEL>  
A:Cross-references: EMBL:X59085; NID:q22281; PTDN:CAA41811.1; PTD:q22282  
A:Note: sequence extracted from NCBI backbone (NCBIN:71282, NCBIPI:71286)

Query Match 100.0%; Score 350; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 6.5e-29;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDDNHHNHGHHKSGQCVRRCDPRWHPRLCEQREEREKROERSRHEADRSGEGSS 60  
Db 25 EDDNHHNHGHHKSGQCVRRCDPRWHPRLCEQREEREKROERSRHEADRSGEGSS 84  
RESULT 2  
B53234  
vicilin-like storage protein Gbl-L, embryo - maize  
N:Alternate names: globulin-1L  
C:Species: Zea mays (maize)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 24-Nov-1999  
C:Accession: B53234; S21824  
R:Belanger, F.C.; Kriz, A.L.  
Genetics 129, 863-872, 1991  
A:Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene.  
A:Reference number: A53234; MUID:92090707  
A:Accession: B53234  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1582 <BEL>  
A:Cross-references: EMBL:X59083; NID:q22283; PTDN:CAA41809.1; PTD:q22284  
A:Experimental source: Inbred line W64A6  
A:Note: sequence extracted from NCBI backbone (NCBIPI:71285)  
C:Genetics:  
A:Gene: Gbl-L  
A:Introns: 167/1; 225/3; 252/3; 349/3  
C:Superfamily: glycinin

```
Query Match          100.0%; Score 350; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.5e-28;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 60
    |||
Db 25 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 84

RESULT 3
vicillin-like storage protein G1b1-S, embryo - maize
C:Species: Zea mays (maize)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
C:Accession: S21825
R:Kriz, A.L.
Submitted to the EMBL Data Library, April 1991
A:Reference number: S21823
A:Accession: S21825
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <R1>
A:Cross-references: EMBL:X59084; NID:g22285; PIDN:CAA41810.1; PID:g22287
C:Genetics:
A:Gene: G1b1-S
A:Introns: 170/1; 195/2; 222/2; 319/2
C:Superfamily: glycIn

Query Match          98.9%; Score 346; DB 2; Length 540;
Best Local Similarity 98.3%; Pred. No. 6e-28;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 60
    |||
Db 25 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 84

RESULT 4
globulin-1S, GLB1S - maize
C:Species: Zea mays (maize)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: A53234; A43642
R:Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism of the maize globulin-1 gene.
A:Reference number: A53234; MUID:92090707
A:Accession: A53234
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <BEL>
A:Experimental source: Inbred line Va 26
A:Note: sequence extracted from NCBI backbone (NCBIN:71280, NCBI:P:71284)
R:Kriz, A.L.
Biochem. Genet. 27, 239-251, 1989
A:Title: Characterization of embryo globulins encoded by the maize GLB genes.
A:Reference number: A43642; MUID:89374022
A:Accession: A43642
A:Status: preliminary
A:Molecule type: protein
A:Residues: 87-100 <KR1>
C:Superfamily: glycIn

Query Match          98.9%; Score 346; DB 2; Length 573;
Best Local Similarity 98.3%; Pred. No. 6.3e-28;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 60
    |||
Db 25 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 84
```

```
RESULT 5
T02258
globulin1 - maize
C:Species: Zea mays (maize)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 29-Oct-1999
C:Accession: T02258
R:Bhatramakl, D.; Kriz, A.L.
Submitted to the EMBL Data Library, May 1995
A:Description: Nucleotide sequence analysis of a novel globulin1 null allele from the
A:Reference number: Z14643
A:Accession: T02258
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-407 <BHA>
A:Cross-references: EMBL:U028017; NID:g927238; PIDN:AAB60295.1; PID:g927239
A:Experimental source: strain IHP
C:Genetics:
A:Gene: G1b1
A:Introns: 168/1; 226/3; 254/1; 351/1

Query Match          97.7%; Score 342; DB 2; Length 407;
Best Local Similarity 96.7%; Pred. No. 1.2e-27;
Matches 58; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 60
    |||
Db 25 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 84

RESULT 6
T01662
globulin-1 - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 11-Jan-2000
C:Accession: T01662
R:Hilton, H.; Gaut, B.S.
Genetics 150, 863-872, 1998
A:Title: Speciation and domestication in maize and its wild relatives: evidence from
A:Reference number: Z14386; MUID:98429537
A:Accession: T01662
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-236 <HIL>
A:Cross-references: EMBL:AF064222; NID:g3414836; PIDN:ACC31465.1; PID:g3414837
A:Experimental source: subspecies parviglumis
C:Genetics:
A:Introns: 166/1; 224/3
C:Superfamily: glycIn

Query Match          86.6%; Score 303; DB 2; Length 236;
Best Local Similarity 88.3%; Pred. No. 6.8e-24;
Matches 53; Conservative 1; Mismatches 0; Indels 6; Gaps 1;

QY 1 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREEEREKROERSRHEADDRSGGSS 60
    |||
Db 25 EDDNNHHHGKSGQCVRCEDRPMHQRPRCLDQCREE-----EFSRHEADDRSGGSS 78

RESULT 7
S35221
globulin Bgl precursor - barley
C:Species: Hordeum vulgare (barley)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S35221
R:Beck, G.R.; Chamberlain, A.K.; Ho, T.H.D.
Mol. Gen. Genet. 239, 209-218, 1993
A:Title: Barley embryo globulin 1 gene, Bgl1: characterization of cDNA, chromosome ma
A:Reference number: S35221; MUID:93287988
A:Accession: S35221
A:Molecule type: mRNA
```



Db 834 HHHHSHKII-----GKKKHQEPDEDDDEEKEKKEKKED 873

## RESULT 12

T28872

hypothetical protein R04E5.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T28872

R:Miller, N.

Submitted to: the EMBL Data Library, December 1995

A:Description: The sequence of C. elegans cosmid R04E5.

A:Reference number: Z20535

A:Accession: T28872

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-997 &lt;MIL&gt;

A:Cross-references: EMBL:U41538; PIDN:AAC48181.1; GSPDB:GN00028; CESP:R04E5.8

A:Experimental source: strain Bristol N2; clone R04E5

C:Genetics:

A:Gene: CESP:R04E5.8

A:Map position: X

A:Introns: 216/3; 234/3; 255/2; 305/1; 669/3; 891/1; 986/2

Query Match 20.4%; Score 71.5; DB 2; Length 997;  
Best Local Similarity 32.0%; Pred. No. 7.2;

Matches 16; Conservative 7; Mismatches 20; Indels 7; Gaps 1;

QY 6 HHHGHSKSGCVRCEDRPMHQRPRCLQCEEREKROERSRHEADRGE 55

Db 913 HHHRGHHHCPRRHHNODRNRHNR-----HDGNRHQNDRSRHHNODRN 955

## RESULT 13

A54660

histidine rich calcium binding protein - human

C:Species: Homo sapiens (man)

C:Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 05-Nov-1999

C:Accession: A54660

R:Hofmann, S.L.; Topham, M.; Hsieh, C.L.; Francke, U.

Genomics 9, 656-669, 1991

A:Title: cDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and its

A:Reference number: A54660; M0ID:91244309

A:Accession: A54660

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-699 &lt;HOF&gt;

A:Cross-references: GB:M60052; NID:q183918; PIDN:AAA88071.1; PID:q183919

C:Genetics:

A:Gene: GDB:HRC

A:Cross-references: GDB:126369; OMIM:142705

A:Map position: 19q13.3-19q13.3

C:Keywords: calcium binding

Query Match 20.3%; Score 71; DB 2; Length 699;  
Best Local Similarity 24.2%; Pred. No. 5.9;

Matches 22; Conservative 7; Mismatches 28; Indels 34; Gaps 3;

QY 1 EDDNNHHNG-----GHKS-----GQCVRCEDRPMH----- 26

Db 413 EVDNHHHHHVRPEDEEVSALGHAQPSHRQSHODETGHGSGSIKEMSHNPGRHTVVK 472

QY 27 QPRRCLEQCKEEREKROERSRHEADRSGE 57

Db 473 DRSHLRKDDSEKEKEEDPGSHEDDESSE 503

## RESULT 14

F71446

hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: columbia  
C:Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 05-Dec-1998

C:Accession: F71446

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D

avanagh, T.; Hempel, S.; Kotter, P.; Entlian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgaden

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;

C.; Chalwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t

A:Reference number: A71400; M0ID:98121113

A:Accession: F71446

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-144 &lt;BEV&gt;

A:Cross-references: GB:297343; NID:g2245073; PID:e327076; PID:g2245125

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 20.0%; Score 70; DB 2; Length 144;  
Best Local Similarity 28.8%; Pred. No. 1.9;

Matches 19; Conservative 9; Mismatches 20; Indels 18; Gaps 3;

QY 4 NHHHGHKS-----GQ-----CVRCEDRP-----WHQPRCLQCEEREKROE 45

Db 43 NHHNHQDNSYVGQPHFLDSCFLCKKRLGDNDLFWYGRDIPFCSEECREQIERDEA 102

QY 46 RSRREA 51

Db 103 KEKKQS 108

## RESULT 15

A42566

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively sp

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Sep-1998

C:Accession: A42566

R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Pathi, S.; Simeron, S.; Maroufi, A.;

Science 257, 389-395, 1992

A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-

A:Reference number: A42566; M0ID:92335886

A:Accession: A42566

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-2339 &lt;WIL&gt;

A:Experimental source: IMR32, hippocampus

A:Note: sequence extracted from NCBI backbone (NCBIP:109168)

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 20.0%; Score 70; DB 2; Length 2339;  
Best Local Similarity 29.4%; Pred. No. 21;

Matches 25; Conservative 6; Mismatches 14; Indels 40; Gaps 5;

QY 4 NHHHGHKSQGCVRCEDRPMHQRPRCLP-----OC 35

Db 2050 HHHHH-----RCHRR-RDR-----KQRSLEKPSLSADMDGAPSAVGLPFGQPTQC 2098

QY 36 REEREKROERSRHEADRSGEGSS 60

Db 2099 R-RERERROERGRSGERHQPSSSSS 2122

Search completed: March 1, 2001, 16:10:43  
Job time: 1074 sec